

GenCore version 5.1.4.D5\_4578  
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OM protein - protein search, using sw model

Run on: March 24, 2003, 15:45:24 ; Search time 11.0303 Seconds

(without alignments)  
977.656 Million cell updates/sec

Title: US-09-988-971-2\_COPY\_2\_261

Sequence: 1 GSIPLSRKSLPSPSLSSVQ.....RESLSPYSLNDAVSLDA 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID         | Description         |
|------------|-------|-------------|--------|------------|---------------------|
| 1          | 374.5 | 27.8        | 511    | LYN_HUMAN  | P07948 homo sapien  |
| 2          | 371.5 | 27.6        | 511    | LYN_MOUSE  | P25511 mus musculus |
| 3          | 371.5 | 27.6        | 511    | LYN_RAT    | Q07014 ratu         |
| 4          | 364.5 | 27.1        | 526    | HCK_HUMAN  | P08631 homo sapien  |
| 5          | 362   | 26.9        | 504    | HCK_MACACA | Q95M30 macaca fasc  |
| 6          | 356.5 | 26.5        | 504    | BLK_HUMAN  | P51451 homo sapien  |
| 7          | 356   | 26.4        | 524    | HCK_MOUSE  | P08103 mus musculus |
| 8          | 355.5 | 26.4        | 503    | HCK_RAT    | P50545 ratu         |
| 9          | 345.5 | 25.7        | 498    | BLK_MOUSE  | P16277 mus musculus |
| 10         | 344   | 25.6        | 508    | LYN_HUMAN  | P06239 homo sapien  |
| 11         | 342.5 | 25.4        | 508    | LCK_MOUSE  | P06240 mus musculus |
| 12         | 337   | 25.0        | 507    | LCK_CHICK  | P42683 gallus gall  |
| 13         | 323.5 | 24.0        | 537    | YES_XENLA  | P10936 xenopus lae  |
| 14         | 321   | 23.8        | 541    | YES_CHICK  | P09324 gallus gall  |
| 15         | 319.5 | 23.7        | 536    | LYN_HUMAN  | P06241 homo sapien  |
| 16         | 319.5 | 23.7        | 543    | YES_HUMAN  | P07947 homo sapien  |
| 17         | 316.5 | 23.5        | 529    | LYN_HUMAN  | P07947 homo sapien  |
| 18         | 315   | 23.4        | 544    | YES_XENLA  | P27447 xiphophorus  |
| 19         | 314.5 | 23.4        | 536    | LYN_XENLA  | P13406 xenopus lae  |
| 20         | 313   | 23.3        | 528    | YES_AVISY  | P00527 avian sarco  |
| 21         | 313   | 23.3        | 533    | LYN_MOUSE  | P33688 mus musculus |
| 22         | 309.5 | 23.0        | 536    | LYN_XIPHE  | P27446 xiphophorus  |
| 23         | 309.5 | 23.0        | 541    | LYN_MOUSE  | P04736 mus musculus |
| 24         | 307   | 22.8        | 517    | LYN_MOUSE  | P14234 mus musculus |
| 25         | 305   | 22.7        | 535    | LYN_CHICK  | Q02977 gallus gall  |
| 26         | 304   | 22.6        | 539    | YES_CANEA  | Q28823 canis fami   |
| 27         | 301.5 | 22.4        | 533    | LYN_CHICK  | Q05876 gallus gall  |
| 28         | 299   | 21.8        | 506    | SRK4_SPOLA | P42690 spingilla 1  |
| 29         | 290.5 | 21.6        | 526    | LYN_MOUSE  | P00525 avian sarco  |
| 30         | 290.5 | 21.6        | 532    | LYN_MOUSE  | P00523 avian sarco  |
| 31         | 290.5 | 21.6        | 552    | LYN_MOUSE  | P00528 drosophila   |
| 32         | 290.5 | 21.6        | 557    | LYN_MOUSE  | P14085 avian sarco  |
| 33         | 290.5 | 21.6        | 587    | LYN_MOUSE  | P15054 avian sarco  |

|    |       |      |     |            |                     |
|----|-------|------|-----|------------|---------------------|
| 34 | 288.5 | 21.4 | 568 | SRC_AVISY  | P14084 avian sarco  |
| 35 | 281.5 | 20.9 | 535 | SRC_RAT    | Q9wud8 ratu         |
| 36 | 280.5 | 20.8 | 526 | SRC_RSISR  | P00524 rous sarcom  |
| 37 | 280.5 | 20.8 | 535 | SRC_HUMAN  | P12931 homo sapien  |
| 38 | 280   | 20.8 | 509 | STK_HYDAT  | P17713 hydra actin  |
| 39 | 278.5 | 20.7 | 531 | SRC2_XENLA | P1316 xenopus lae   |
| 40 | 277.5 | 20.6 | 526 | SRC_RSVP   | P00526 rous sarcom  |
| 41 | 275.5 | 20.5 | 540 | SRC_MOUSE  | P05488 mus musculus |
| 42 | 273.5 | 20.3 | 531 | SRC2_XENLA | P13115 xenopus lae  |
| 43 | 272.5 | 20.2 | 526 | SRC_RSVP   | P25020 rous sarcom  |
| 44 | 271   | 20.1 | 505 | SRK1_SPOLA | P42686 spingilla 1  |
| 45 | 261   | 19.4 | 545 | FGR_FSVGR  | P00544 feline sarc  |

## ALIGNMENTS

```

RESULT 1
LYN_HUMAN
ID LYN_HUMAN STANDARD; PRT; 511 AA.
AC P07948;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase LYN (EC 2.7.1.112).
GN LYN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP MEDLINE=9712710; PubMed=3561390;
RA Yamashita Y., Fukushige S.-I., Semba K., Sukegawa J., Miyajima N.,
RA Matsubara K.-I., Yamamoto T., Toyoshima K.;
RT "The yes-related cellular gene lyn encodes a possible tyrosine kinase
RT similar to p56lck."
RL Mol. Cell. Biol. 7:237-243(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94171041; PubMed=8125304;
RA Rider L.G., Raben N., Miller L., Jelsma C.;
RT "The CDNs encoding two forms of the LYN protein tyrosine kinase are
RT expressed in rat mast cells and human myeloid cells."
RL Gene 138:219-222(1994).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS, LYN A (SHOWN HERE) AND LYN B;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-----
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DR EMBL: M16038; AA59540.1; -
DR EMBL: M79321; AA50019.1; -
DR PIR: A26719; TVHILY.
DR HSSP: P08631; IAD5.
DR MIM: 165120; -
DR InterPro: IPR000719; Euk_pkinae.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00017; SH2; 1.

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DR Pfam; PF00018; SH3; 1.  
 DR Pfam; PF00069; kinase; 1.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PRODOM; PD000001; Euk\_kinase; 1.  
 DR PRODOM; PD000066; SH3; 1.  
 DR PRODOM; PD000093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TYKc; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;  
 KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;  
 KW Palmitate; Lipoprotein; Alternative splicing.  
 FT INIT MET 0  
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).  
 FT LIPID 2 2 PALMITATE (BY SIMILARITY).  
 FT DOMAIN 62 122 SH3.  
 FT DOMAIN 128 225 SH2.  
 FT NP BIND 246 500 PROTEIN KINASE.  
 FT BINDING 252 260 ATP (BY SIMILARITY).  
 FT ACT SITE 274 274 ATP (BY SIMILARITY).  
 FT MOD RES 366 366 BY SIMILARITY.  
 FT MOD RES 396 396 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD RES 507 507 PHOSPHORYLATION (BY SIMILARITY).  
 FT VARSPLIC 22 42 MISSING (IN ISOFORM LYN B).  
 SO SEQUENCE 511 AA; 58442 MW; 8419CD461204E364 CRC64.

Query Match 27.8%; Score 374.5; DB 1; Length 511;  
 Best Local Similarity 40.3%; Pred. No. 2,7e-24;  
 Matches 81; Conservative 36; Mismatch 75; Indels 9; Gaps 3;

OY 5 SRRKSLPSPSLSSVOGGPVTWEAERSKATVALGSGFPAAGAEILRLPEPTLYSED 64  
 DB 37 SNKQGRPVE-SQLLPGQRCTDPPEQGDIVVALYDDIHDDLSFKGEEKKVLSEH 95  
 OY 65 GDMWTVLSEVSGREYNIPSVHAKV---SHGWLVEGLSEKKEELLIPGPGATLIR 120  
 DB 96 GEWWKAKSLITKEGFIIPSNVAKNLTLTEWEPFKDITRKDKERQLAPNGSAGELAR 155  
 OY 121 ESOTRRGYSLSVRLSRPASWDRIHRYHICLDNGMWYIPRLTFPSLQALVDVYSLEAD 180  
 DB 156 ESETLKGSTLSVRDPDVHGVDTIKYKIKRSLDNGGYISPRITFPCISDMIKHYQKQND 215  
 OY 181 DICLLKEPCVLDQRAGPLPK 201  
 DB 216 GLCRLEKACI---SPKPK 232

## RESULT 2

## LYN\_MOUSE

ID LYN\_MOUSE STANDARD; PRT; 511 AA.  
 AC P25911; 062127; 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase LYN (EC 2.7.1.112).  
 GN LYN.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP MEDLINE FROM N.A.  
 RX MEDLINE=91260688; PubMed=1710766;  
 RA Stanley E., Ralph S.J., McEwen S., Boulet I., Holtzman D.A.,  
 RA Lock P., Dunn A.R.;  
 RT "Alternatively spliced murine lyn mRNAs encode distinct proteins";  
 RL Mol. Cell. Biol. 11:3399-3406(1991).

RN [2]  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE=91203857; PubMed=2017160;  
 RA Yi T., Boelen J.B., Inle J.N.;  
 RT "Hematopoietic cells express two forms of lyn kinase differing by 21  
 RT amino acids in the amino terminus";  
 RL Mol. Cell. Biol. 11:2391-2398(1991).  
 RN [3]  
 RX SEQUENCE OF 363-431 FROM N.A.  
 RX MEDLINE=90152381; PubMed=2482828;  
 RA Wilks A.F., Kudan R.R., Hovens C.M., Ralph S.J.;  
 RT "The application of the polymerase chain reaction to cloning members  
 RT of the protein tyrosine kinase family";  
 RL Gene 85:67-74(1989).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; LYN A (SHOWN HERE) AND LYN B;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN B-LYMPHOID AND  
 CC MYELOID CELLS.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 CC -----  
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 DR EMBL; M64608; AAA39470.1; -  
 DR EMBL; M57696; AAA39471.1; -  
 DR EMBL; M57697; AAA39472.1; -  
 DR EMBL; M33426; AAA40017.1; -  
 DR PIR; A39719; A39719.  
 DR HSSP; P08631; 1AD5.  
 DR MGD; MGI:96892; LYN.  
 DR InterPro; IPR000719; Euk\_kinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; TYR\_kinase.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR Pfam; PF00069; kinase; 1.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PRODOM; PD000001; Euk\_kinase; 1.  
 DR PRODOM; PD000066; SH3; 1.  
 DR PRODOM; PD000093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TYKc; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;  
 KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;  
 KW Palmitate; Lipoprotein; Alternative splicing.  
 FT INIT MET 0  
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).  
 FT LIPID 2 2 PALMITATE (BY SIMILARITY).  
 FT DOMAIN 62 122 SH3.  
 FT DOMAIN 128 225 SH2.  
 FT NP BIND 246 500 PROTEIN KINASE.  
 FT BINDING 252 260 ATP (BY SIMILARITY).  
 FT ACT SITE 274 274 ATP (BY SIMILARITY).  
 FT MOD\_RES 366 366 BY SIMILARITY.  
 FT MOD\_RES 396 396 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

FT MOD.RES 507 507 PHOSPHORYLATION (BY SIMILARITY).  
 FT VARSPIC 24 44 MISSING (IN ISOFORM LYN B).  
 FT CONFLICT 76 76 I -> F (IN REF. 2).  
 FT CONFLICT 160 160 L -> I (IN REF. 2).  
 FT CONFLICT 278 278 P -> L (IN REF. 2).  
 FT CONFLICT 390 390 V -> I (IN REF. 2).  
 FT CONFLICT 414 414 I -> F (IN REF. 3).  
 FT CONFLICT 424 424 D -> N (IN REF. 3).  
 FT CONFLICT 431 431 L -> P (IN REF. 3).  
 SQ SEQUENCE 511 AA; 58681 MW; 3935221CCGCGC0609 CRCC4;  
 Query Match 27.6%; Score 371.5; DB 1; Length 511;  
 Best Local Similarity 40.8%; Pred. No. 4,9e-24;  
 Matches 82; Conservative 33; Mismatches 77; Indels 9; Gaps 3;  
 QY 5 SRRKSLPSSVSSVGGQGVYMEARSKATAVAFSPAGPAPALSLRGEPLTVSEED 64  
 DB 37 SNKQQRVPVEF-HLPGQRFOYKQPEBEGQIVVALLPYDGHFDLSFKGKGMKYLEEH 95  
 QY 65 GDMWTVLSEVSGREYNIPSVHAKV---SHGWLVEGLSREKAEELLPLPGNGAPFLIR 120  
 DB 96 GEMWKAISLSKREGEFIPSNVYAKVNTLETMEFMDITRKDAERQLAPGNSAGAPFLIR 155  
 QY 121 ESQTRGSGYSVLSRPSASMDRIHRYHICLDMGWLTPSPRLTPEPQLALVDHYSELD 180  
 DB 156 ESEFLKGSFSLVSDVDPMHGDVIAKHKIKSLDNGYIISRIITFPCLSDIMIKHYKQSD 215  
 QY 181 DICLLKEPCVLOKAGPLPGK 201  
 DB 216 GLCRRLERKACT---SPKPK 232  
 RESULT 3  
 LYN\_RAT STANDARD; PRT; 511 AA.  
 ID LYN\_RAT  
 AC 007014; 063320; Created  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase LYN (EC 2.7.1.112).  
 GN LYN.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxId=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Minoguchi K., Nishikata H., Siraganian R.P.;  
 RT "Bacterially expressed rat p56lyn binds several proteins in rat  
 RT basophilic leukemia cells including pp72, a tyrosine phosphorylated  
 RT protein prominent in activated cells.";  
 RN J. Immunol. 150:222-222(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=94171041; PubMed=8125304;  
 RA Rider L.G., Raben N., Miller L., Jelsema C.;  
 RT "The CDNA encoding two forms of the LYN protein tyrosine kinase are  
 RT expressed in rat mast cells and human myeloid cells.";  
 RN Gene 138:219-222(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=9742484; PubMed=9295361;  
 RA Vonakis B.M., Chen H., Haleem-Smith H., Metzger H.;  
 RT "The unique domain as the site on LYN kinase for its constitutive  
 RT association with the high affinity receptor for IgE.";  
 RN J. Biol. Chem. 272:24072-24080(1997).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, LYN A (SHOWN HERE) AND LYN B;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN B-LYMPHOID AND  
 CC MYELOID CELLS.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC

CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
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 CC -----  
 DR EMBL: L14951; AAA41549.1; -;  
 DR EMBL: L14782; AAA20944.1; -;  
 DR EMBL: L14823; AAA20945.1; -;  
 DR EMBL: AF000300; AAB71344.1; -;  
 DR EMBL: AF000301; AAB71345.1; -;  
 DR EMBL: AF000302; AAB71346.1; -;  
 DR HSSP: P08631; 1AD5.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR000980; SH2.  
 DR InterPro: IPR001452; SH3.  
 DR InterPro: IPR001451; Tyr\_pkinase.  
 DR Pfam: PF00017; SH2; 1.  
 DR Pfam: PF00018; SH3; 1.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PR00452; SH3DOMAIN.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR ProDom: PD000066; SH3; 1.  
 DR ProDom: PD000093; SH2; 1.  
 DR SMART: SM00252; SH2; 1.  
 DR SMART: SM00326; SH3; 1.  
 DR SMART: SM00219; tyrc; 1.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS50001; SH2; 1.  
 DR PROSITE: PS50002; SH3; 1.  
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;  
 KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;  
 KW Palmitate; Lipoprotein; Alternative splicing.  
 FT INTR MET 0  
 FT LIPID 1 1  
 FT DOMAIN 1 2  
 FT LIPID 2 2  
 FT DOMAIN 62 122  
 FT DOMAIN 128 225  
 FT NP\_BIND 252 500  
 FT BINDING 274 274  
 FT ACT\_SITE 366 366  
 FT MOD\_RES 366 366  
 FT VARSPIC 507 507  
 FT CONFLICT 24 44  
 FT CONFLICT 230 230  
 FT CONFLICT 307 307  
 FT CONFLICT 418 418  
 SQ SEQUENCE 511 AA; 58529 MW; 24425E229CD43ED CRCC4;  
 Query Match 27.6%; Score 371.5; DB 1; Length 511;  
 Best Local Similarity 40.8%; Pred. No. 4,9e-24;  
 Matches 82; Conservative 33; Mismatches 77; Indels 9; Gaps 3;  
 QY 5 SRRKSLPSSVSSVGGQGVYMEARSKATAVAFSPAGPAPALSLRGEPLTVSEED 64  
 DB 37 SNKQQRVPVEF-HLPGQRFOYKQPEBEGQIVVALLPYDGHFDLSFKGKGMKYLEEH 95  
 QY 65 GDMWTVLSEVSGREYNIPSVHAKV---SHGWLVEGLSREKAEELLPLPGNGAPFLIR 120  
 DB 96 GEMWKAISLSKREGEFIPSNVYAKVNTLETMEFMDITRKDAERQLAPGNSAGAPFLIR 155  
 QY 121 ESQTRGSGYSVLSRPSASMDRIHRYHICLDMGWLTPSPRLTPEPQLALVDHYSELD 180



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CC -----  
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DR EMBL, BC014435, AAH14435.1; -  
DR EMBL, AK026432, BAB15482.1; -  
DR EMBL, AL049539, CAB75606.1; -  
DR EMBL, X58741, CAA41565.2; -  
DR EMBL, X58742, CAA41565.2; JOINED.  
DR EMBL, X58743, CAA41565.2; JOINED.  
DR PIR, A27812, TVHUC.  
DR PDB, 2HCK, 20-AUG-97.  
DR PDB, 3HCK, 15-OCT-97.  
DR PDB, 4HCK, 17-JUN-98.  
DR PDB, 5HCK, 17-JUN-98.  
DR PDB, 1AD5, 15-MAY-97.  
DR PDB, 1BUI, 11-NOV-98.  
DR Genew, HGNC:4840, HCK.  
DR MIM, 142370, -  
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DR InterPro, IPR001452, SH3.  
DR InterPro, IPR002290, Ser\_thr\_pkinase.  
DR InterPro, IPR001245, Tyr\_pkinase.  
DR Pfam, PF00017, SH2, 1.  
DR Pfam, PF00018, SH3, 2.  
DR Pfam, PF00069, pkinase, 4.  
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DR SMART, SM00252, SH2, 1.  
DR SMART, SM00326, SH3, 1.  
DR SMART, SM00220, S\_TKc, 1.  
DR SMART, SM00219, TYKc, 1.  
DR PROSITE, PS00107, PROTEIN KINASE ATP, 1.  
DR PROSITE, PS00109, PROTEIN KINASE TYR, 1.  
DR PROSITE, PS50011, PROTEIN\_KINASE\_DOM, 1.  
DR PROSITE, PS50001, SH2, 1.  
DR PROSITE, PS50002, SH3, 1.  
KW Tyrosinase: Tyrosine-protein kinase; phosphorylation; ATP-binding;  
KW Myristate; SH2 domain; SH3 domain; Alternative initiation;  
KW 3D-structure.  
KM CHAIN 1 526  
FT INIT MET 22 526 TYROSINE-PROTEIN KINASE P59-HCK.  
FT DOMAIN 78 138 FOR ISOFORM P59-HCK.  
FT DOMAIN 144 241 SH2.  
FT NP BIND 266 276 PROTEIN KINASE.  
FT BINDING 290 290 ATP.  
FT ACT\_SITE 381 381  
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).  
FT MOD\_RES 411 411 C -> S (IN REF. 1).  
FT CONFLICT 24 24 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT CONFLICT 144 144 W -> R (IN REF. 4).  
SQ SEQUENCE 526 AA; 59559 MW; 847B877A0A61175 CRC64;

Query Match 27.18; Score 364.5; DB 1; Length 526;  
Best Local Similarity 42.28; Pred. No. 2e-23;  
Matches 78; Conservative 31; Mismatches 69; Indels 7; Gaps 2;

Qy 11 PPSLSSVGGCPVTMEAKSKATVAAGSPAGPAEALRGEELIVSEDDQMTV 70  
Db 61 PGRSHNS--NTFGIRAGSEDIIVALYDEALHHEDLSFGQGMVVLSESEWKA 117  
Qy 71 LSEVSGREINISGVAVKY---SHGWLVEGLSREKAEILLPGNPGGAPLIRSQTR 126  
Db 118 RSLATREGEYISNYVARVDLFTTEWFFKGISRDAERQLALPGMGLGFMIRDSERTK 177

Qy 127 GSYSLSVRLSPASMDRIHRYHICLDNGMLYSRLTFPSLQALVDHYSLEADICCL 186  
Db 178 GSYSLSVRLSPASMDRIHRYHICLDNGMLYSRLTFPSLQALVDHYSLEADICCL 237  
Qy 187 KPCV 191  
Db 238 SVPCW 242

# RESULT 5

HCK\_MACFA STANDARD; PRT; 504 AA.

AC 095630;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (p56-HCK) (Hemopoietic cell  
DE kinase).  
GN HCK.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Macaca.  
OX NCBI\_Taxid=9541;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Picard C.;  
RL Thesis (2001), University of Marseille, France.  
CC -!- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC  
CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO  
CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE  
CC DEGRANULATION PROCESS OF NEUTROPHILS (By similarity).

CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate.  
CC -!- SUBCELLULAR LOCATION: Membrane-associated (By similarity).  
CC -!- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
CC SUBFAMILY.

CC -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL, AJ320181, CAC44031.1; -  
CC InterPro, IPR000719, Euk\_pkinase.  
CC InterPro, IPR000980, SH2.  
CC InterPro, IPR001452, SH3.  
CC InterPro, IPR001245, Tyr\_pkinase.

DR Pfam, PF00017, SH2, 1.  
DR Pfam, PF00018, SH3, 1.  
DR Pfam, PF00069, pkinase, 1.  
DR Prodom, PD000066, SH3, 1.  
DR Prodom, PD000093, SH2, 1.  
DR Prodom, PD000109, PROTEIN KINASE ATP, 1.  
DR PROSITE, PS00107, PROTEIN KINASE TYR, 1.  
DR PROSITE, PS50011, PROTEIN\_KINASE\_DOM, 1.  
DR PROSITE, PS50001, SH2, 1.  
DR PROSITE, PS50002, SH3, 1.

KW Tyrosinase; Tyrosine-protein kinase; phosphorylation; ATP-binding;  
KW Myristate; SH2 domain; SH3 domain.  
FT DOMAIN 56 116 SH2.  
FT DOMAIN 122 219 SH3.  
FT NP BIND 240 254 PROTEIN KINASE.  
FT BINDING 268 268 ATP (BY SIMILARITY).  
FT ACT\_SITE 359 359 ATP (BY SIMILARITY).  
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).

FT MOD RES 389 389 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 SQ SEQUENCE 504 AA: 57096 MW: 53829322DD3423 CRC64;  
 Query Match 26.9%; Score 362; DB 1; Length 504;  
 Best Local Similarity 45.9%; Pred. No. 3, 1e-23;  
 Matches 73; Conservative 29; Mismatches 53; Indels 4; Gaps 1;  
 QY 37 VALGSPAGPAELSLRLGEPPLTIVSEDDGMMWTVLSVSGREYNIPSVYAVKY---SHG 92  
 DB 62 VALDYEAHHEHDLSEFGKQGVWVLEESGEWKKRSIATRKGYIPSNVYAVRDSLETSE 121  
 QY 93 WVEGLSREKAEELLIPGPGAFILRESQTRGSYSLSVRLSPASMDRIRYHICL 152  
 DB 122 WPKGISRKDAERQLAPGNMGSSFNIDSEITKGSYSLSVADYPRGQGVYHXYKIRTL 181  
 QY 153 DNGWLYISPRLPSPLOALVDHYSEIADICLLKEPCV 191  
 DB 182 DNGGFYISPRSTFSTLQELVDHYKKGSDGLCQKLSPVCV 220  
 RESULT 6  
 BLK\_HUMAN STANDARD; PRT; 504 AA.  
 ID BLK\_HUMAN  
 AC P51451; Q16291;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase Blk (EC 2.7.1.112) (B lymphocyte kinase) (p55-  
 DE BLK).  
 GN Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95121078; PubMed=7822795;  
 RA Islam K.B., Rabbani H., Larsson C., Sanders R., Smith C.I.;  
 RT "Molecular cloning, characterization, and chromosomal localization of  
 RT a human lymphoid tyrosine kinase related to murine Blk.";  
 RL J. Immunol. 154:1265-1272 (1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95148218; PubMed=7845672;  
 RA Drebin J.A., Hartzell S.W., Griffin C., Campbell M.J.,  
 RA Niederhuber J.E.;  
 RT "Molecular cloning and chromosomal localization of the human homologue  
 RT of a B-lymphocyte specific protein tyrosine kinase (blk).";  
 RL Oncogene 10:477-486 (1995).  
 CC -1- FUNCTION: BLK MAY FUNCTION IN A SIGNAL TRANSDUCTION PATHWAY THAT  
 CC IS RESTRICTED TO B LYMPHOID CELLS.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC  
 CC EMBL: Z3398; CA83965.1; -;  
 CC EMBL: S7617; AAB3265.1; -;  
 CC HSSP: P16277; BLK.  
 CC Genew: HGNC:1057; BLK.  
 CC MIM: 191305; -;  
 CC InterPro: IPR000719; Blk\_kinase.  
 CC InterPro: IPR000980; SH2.

DR InterPro: IPR001452; SH3.  
 DR InterPro: IPR001245; Tyr\_kinase.  
 DR Pfam: PF00017; SH2; 1.  
 DR Pfam: PF00018; SH3; 1.  
 DR Pfam: PF00069; kinase; 1.  
 DR PRINTS: PRO0401; SH2DOMAIN.  
 DR PRINTS: PRO0452; SH3DOMAIN.  
 DR PRINTS: PRO0109; TYRKINASE.  
 DR ProDom: PD000001; Euk\_kinase; 1.  
 DR ProDom: PD000066; SH3; 1.  
 DR ProDom: PD000093; SH2; 1.  
 DR SMART: SM00252; SH2; 1.  
 DR SMART: SM00326; SH3; 1.  
 DR SMART: SM00219; Tyrc; 1.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE: PS00109; PROTEIN KINASE TYR; FALSE\_NEG.  
 DR PROSITE: PSS0011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PSS0001; SH2; 1.  
 DR PROSITE: PSS0002; SH3; 1.  
 KW Tyrosine-protein kinase; phosphorylation; transferase; ATP-binding;  
 KW Myristate; SH2 domain; SH3 domain.  
 FT INIT MET 0 0  
 FT LIPID 1 1  
 FT DOMAIN 57 117 MYRISTATE (BY SIMILARITY).  
 FT DOMAIN 123 219 SH3.  
 FT DOMAIN 240 493 PROTEIN KINASE.  
 FT NP\_BIND 246 254 ATP (BY SIMILARITY).  
 FT BINDING 268 268 ATP (BY SIMILARITY).  
 FT ACT\_SITE 359 359 BY SIMILARITY.  
 FT MOD\_RES 388 388 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT CONFLICT 286 286 M -> V (IN REF. 2).  
 FT CONFLICT 406 406 I -> Y (IN REF. 2).  
 SQ SEQUENCE 504 AA: 57607 MW: 581050E7370C8 CRC64;  
 Query Match 26.5%; Score 356.5; DB 1; Length 504;  
 Best Local Similarity 44.2%; Pred. No. 9e-23;  
 Matches 76; Conservative 24; Mismatches 67; Indels 5; Gaps 2;  
 QY 24 PYTMAERSKATVALGSPAGPAELSLRLGEPPLTIVSEDDGMMWTVLSVSGREYNIP 83  
 DB 50 PDEHLDLDDHGFVALVDYTDANNDRDQLMKGKGLQVKGTDWMLRSIVTREGYVPS 109  
 QY 84 VHVAYVS---HGMVGEISREKAEELLIPGPGAFILRESQTRGSYSLSVRLSPA 139  
 DB 110 NFVAVESLEMERFPRSGQREARQLAPINKAGSFLIRSEITNGAFTSLVK-DVTT 168  
 QY 140 SMDRIRYHICLDNGWLYISPRLPSPLOALVDHYSEIADICLLKEPCV 191  
 DB 169 QGELLKHVKIKRCDEGGYISPRIPSLQALVDHYSKKGDGLCQRLTLCV 220  
 RESULT 7  
 HCK\_MOUSE STANDARD; PRT; 524 AA.  
 ID HCK\_MOUSE  
 AC P08103;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P55-HCK and P60-HCK)  
 DE (hemopoietic cell kinase) (B-cell/myeloid kinase) (BMK).  
 GN Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN  
 RP SEQUENCE OF 22-524 FROM N.A.  
 RA STRAIN=ICR; TISSUE=Macrophage;  
 RX MEDLINE=88067781; PubMed=3684607;  
 RA Klemenz M.J., McKeicher S.R., Maki R.A.;  
 RT "Nucleotide sequence of the mouse hck gene";  
 RL Nucleic Acids Res. 15:9600-9600 (1987).  
 RN [2]

RP SEQUENCE OF 22-524 FROM N.A.  
 RX MEDLINE=8068587; PubMed=3317404.  
 RA Holzman D.A., Cook W.D., Dunn A.R.;  
 RT "Isolation and sequence of a cDNA corresponding to a src-related gene  
 expressed in murine hemopoietic cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8325-8329(1987).  
 RN (3)  
 RP SEQUENCE OF 1-22 FROM N.A. AND ALTERNATIVE INITIATION.  
 RX MEDLINE=9134263; PubMed=1875927.  
 RA Lock P., Ralph S., Stanley E., Boulet I., Ramsey R., Dunn A.R.;  
 RT "Two isoforms of murine hck, generated by utilization of alternative  
 translational initiation codons, exhibit different patterns of  
 subcellular localization.";  
 RL Mol. Cell. Biol. 11:4363-4370(1991).  
 CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC  
 RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO  
 CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE  
 DEGRANULATION PROCESS OF NEUTROPHILS.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: P59-HCK AND P56-HCK ARE ASSOCIATED WITH  
 MEMBRANES. P59-HCK IS ALSO CYTOSOLIC.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms, p59-HCK (shown here) and p56-  
 HCK; are produced by alternative initiation.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE  
 MYELOID AND B-LYMPHOID LINEAGES.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: Y00487; CAA68544.1; -;  
 DR EMBL: J03023; AAA37305.1; -;  
 DR PIR: A27282; TVMSHC.  
 DR PIR: A39973; A39973.  
 DR HSSP: P08631; IAD5.  
 DR MGD: MGI:96052; HCK.  
 DR InterPro: IPR000719; Euk\_Pkinase.  
 DR InterPro: IPR000980; SH2.  
 DR InterPro: IPR001452; SH3.  
 DR InterPro: IPR001245; Tyr\_Pkinase.  
 DR Pfam: PF00017; SH2; 1.  
 DR Pfam: PF00018; SH3; 1.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR PRINTS: PR00401; SH2DOMAIN.  
 DR PRINTS: PR00452; SH2DOMAIN.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR ProDom: PD000001; Euk\_Pkinase; 1.  
 DR ProDom: PD000066; SH3; 1.  
 DR ProDom: PD000093; SH2; 1.  
 DR SMART: SM00252; SH2; 1.  
 DR SMART: SM00326; SH3; 1.  
 DR SMART: SM00219; Tyrc; 1.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS50001; SH2; 1.  
 DR PROSITE: PS50002; SH3; 1.  
 DR Transferase: Tyrosine-protein kinase; phosphorylation; ATP-binding;  
 KW Myristate; SH2 domain; SH3 domain; Alternative initiation.  
 FT CHAIN 1 524 TYROSINE-PROTEIN KINASE P59-HCK.  
 FT INT MET 22 524 TYROSINE-PROTEIN KINASE P56-HCK.  
 FT DOMAIN 76 136 FOR ISOFORM P56-HCK.  
 FT DOMAIN 142 239 SH2.

FT DOMAIN 260 513 PROTEIN KINASE.  
 FT NP BIND 266 274 ATP (BY SIMILARITY).  
 FT BINDING 288 288 ATP (BY SIMILARITY).  
 FT ACT SITE 379 379 BY SIMILARITY.  
 FT LIPID 2 2 MYRISTATE (BY SIMILARITY).  
 FT LIPID 23 23 MYRISTATE (BY SIMILARITY).  
 FT MOD RES 409 409 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 SQ SEQUENCE 524 AA; 59129 MW; D7F2FD69B38C9706 CRC64;  
 Query Match 26.4%; Score 356; DB 1; Length 524;  
 Best Local Similarity 41.5%; Pred. No. 1e-22;  
 Matches 83; Conservative 33; Mismatches 72; Indels 12; Gaps 4;  
 QY 10 LPSSTSSSSVQGGVWTE---AERKAT-AVALGSFAGAPNELRLRGEPLTVSDG 65  
 DB 51 VPDSTSSKLGKRNNSNMPGFEVGGEDTIVALTDEAHREDLSFQGDQVVLLEAG 110  
 QY 66 DWMTVLSEVSGREYNIPISVHAKV---SHGWLVEGSLREKAEELLPLPGNPGAFILRE 121  
 DB 111 EMMKASRLATKKEGYIPENYVAVNSLETIEWFPKGISRKDARRHLAPGNMLGSPMIRD 170  
 QY 122 SOTRGYSLSVRLSRPASMDRIIRYRHCILNGWLYSPRLFPPLQALVDHYSELAD 181  
 DB 171 SETTKGSYLSVYRDPDPQHGDVYKRYKRTLDGSGFYISPRSTFSSLOELVLYHKXDG 230  
 QY 182 ICLLKEPCVILQRAGPLPGK 201  
 DB 231 LQQLTSVPCV-----SPKPK 246  
 RESULT 8  
 HCK\_RAT  
 ID HCK\_RAT STANDARD; PRT; 503 AA.  
 AC P50545; Q64647;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase HCK (EC 2.7.1.12) (p56-HCK) (Hemopoietic cell  
 kinase).  
 GN HCK.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92109719; PubMed=1764064;  
 RA Okano Y., Sugimoto Y., Fukuoaka M., Matsui A., Nagata K.I., Nozawa Y.;  
 RT "Identification of rat cDNA encoding hck tyrosine kinase from  
 megakaryocytes.";  
 RL Biochem. Biophys. Res. Commun. 181:1137-1144(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Mistral; TISSUE=Spleen;  
 RA Vijaya Gouri B.S., Renu V., Kamarkar S., Swarnu G.;  
 RT "Nucleotide sequence of a cDNA coding for rat hck tyrosine kinase and  
 characterization of its gene product.";  
 RL J. Biosci. 15:117-129(1994).  
 CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC  
 RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO  
 CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE  
 DEGRANULATION PROCESS OF NEUTROPHILS.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: Membrane-associated.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 CC -----  
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CC EMBL, S74141; AAB20754.1; -  
 CC EMBL, M83666; AAA41312.1; -  
 CC EMBL, X62345; CAA44218.1; -  
 CC HSSP, P08631; 1BU1.  
 CC InterPro: IPR000719; Euk\_pkinase.  
 CC InterPro: IPR000980; SH2.  
 CC InterPro: IPR001452; SH3.  
 CC InterPro: IPR001245; Tyr\_pkinase.  
 CC Pfam; PF00017; SH2; 1.  
 CC Pfam; PF00018; SH3; 1.  
 CC Pfam; PF00069; pkinase; 1.  
 CC PRINTS; PR00401; SH2DOMAIN.  
 CC PRINTS; PR00452; SH3DOMAIN.  
 CC PRINTS; PR00109; TYRKINASE.  
 CC ProDom; PD000001; Euk\_pkinase; 1.  
 CC ProDom; PD000065; SH3; 1.  
 CC ProDom; PD000093; SH2; 1.  
 CC SMART; SM00252; SH2; 1.  
 CC SMART; SM00326; SH3; 1.  
 CC SMART; SM00219; TYKIC; 1.  
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 CC PROSITE; PS00109; PROTEIN KINASE\_TYR; 1.  
 CC PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC PROSITE; PS50001; SH2; 1.  
 CC PROSITE; PS50002; SH3; 1.  
 CC Transferrase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;  
 CC Myristate; SH2 domain; SH3 domain.  
 CC DOMAIN 55 115 SH3.  
 CC DOMAIN 121 218 SH2.  
 CC DOMAIN 239 492 PROTEIN KINASE.  
 CC NP\_BIND 245 253 ATP (BY SIMILARITY).  
 CC BINDING 267 267 ATP (BY SIMILARITY).  
 CC ACT\_SITE 358 358 BY SIMILARITY.  
 CC LIPID 2 2 MYRISTATE (BY SIMILARITY).  
 CC MOD\_RES 388 388 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 CC CONFLICT 51 51 F -> V (IN REF. 2).  
 CC CONFLICT 205 205 K -> R (IN REF. 2).  
 CC CONFLICT 306 306 I -> T (IN REF. 2).  
 CC SEQUENCE 503 AA; 57016 MW; 1AFC1F3F0E82FF73 CRC64;

Query Match 26.4%; Score 355.5; DB 1; Length 503;  
 Best Local Similarity 41.4%; Pred. No. 1,1e-22;  
 Matches 84; Conservative 32; Mismatches 72; Indels 15; Gaps 4;

QY 4 PSRRKSLPPSLSSVVOGQPVYMEERKAT-AVALGSPAGPAELSLRLGPLETTYS 62  
 DB 33 PTPSPKLLGPNINSINLPFG-----FVEGSEDTIVVALDYDEALHREDLSFGKQGMVYLE 86  
 QY 63 EDGDMMTVLSEVSGRENNIVSYVAIV-----SHGLVEYGSREKAEELLPGNGAPF 118  
 DB 87 ESGEMKARSLATKKEGIVPSNYVAANVLEETFEFGISRKDAARHLARGMGLSGFM 146  
 QY 119 IRBSQTRGSGYSLVRLSRPASWDRIHRIHCLDNLITISRLTFPSLQALVDHYSSEL 178  
 DB 147 IRDSEITTKGYSLSYRDFDPHGDTYKHYKIRTLDSGGFYISPRSTFSSLOELVHYKKG 206  
 QY 179 ADDICCLKEPCVLRAGAPLPKG 201  
 DB 207 KDGLCKLSTVPCV-----SPKQK 225

RESULT 9  
 BLK\_MOUSE STANDARD; PRT; 498 AA.  
 AC P16277;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tyrosine-protein kinase BLK (EC 2.7.1.112) (B lymphocyte kinase) (p55-  
 DE BLK).  
 GN BLK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=B-cell;  
 RX MEDLINE=90117147; PubMed=2404338;  
 RA Dymecki S.M., Niederhuber J.B., Desiderio S.V.;  
 RT "Specific expression of a tyrosine kinase gene, blk, in B lymphoid  
 RT cells";  
 RL Science 247:332-336(1990).  
 CC [2]  
 CC STRUCTURE BY NMR OF SH2 DOMAIN  
 CC MEDLINE=96224819; PubMed=8639560;  
 CC Mettler W.J., Jelting B., Pryor K., Mueller L., Farmer B.T. II;  
 CC "The three-dimensional solution structure of the SH2 domain from  
 CC p55blk kinase";  
 CC Biochemistry 35:6201-6211(1996).  
 CC -1- FUNCTION: BLK MAY FUNCTION IN A SIGNAL TRANSDUCTION PATHWAY THAT  
 CC IS RESTRICTED TO B LYMPHOID CELLS.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC -1- tyrosine phosphate.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
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 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>  
 CC or send an email to [license@isb-sdb.ch](mailto:license@isb-sdb.ch)).

CC EMBL, M30903; AAA0453.1; -  
 CC PIR, A40092; A40092.  
 CC PDB; 1BLU; 12-MAR-97.  
 CC PDB; 1BLK; 12-MAR-97.  
 CC MGD; MGI:88169; BLK.  
 CC InterPro: IPR000719; Euk\_pkinase.  
 CC InterPro: IPR000980; SH2.  
 CC InterPro: IPR001452; SH3.  
 CC InterPro: IPR001245; Tyr\_pkinase.  
 CC Pfam; PF00017; SH2; 1.  
 CC Pfam; PF00018; SH3; 1.  
 CC Pfam; PF00069; pkinase; 1.  
 CC PRINTS; PR00401; SH2DOMAIN.  
 CC PRINTS; PR00452; SH3DOMAIN.  
 CC PRINTS; PR00109; TYRKINASE.  
 CC ProDom; PD000001; Euk\_pkinase; 1.  
 CC ProDom; PD000065; SH3; 1.  
 CC ProDom; PD000093; SH2; 1.  
 CC SMART; SM00252; SH2; 1.  
 CC SMART; SM00326; SH3; 1.  
 CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 CC PROSITE; PS00109; PROTEIN KINASE\_TYR; FALSE\_NEG.  
 CC PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC PROSITE; PS50001; SH2; 1.  
 CC PROSITE; PS50002; SH3; 1.  
 CC Tyrosine-protein kinase; Phosphorylation; Transferrase; ATP-binding;  
 CC Myristate; SH2 domain; SH3 domain; 3D-structure.  
 CC LIPID 0 0 MYRISTATE (BY SIMILARITY).  
 CC INIT\_MET 1 1 SH3.  
 CC DOMAIN 51 111 SH2.  
 CC DOMAIN 117 213 PROTEIN KINASE.  
 CC DOMAIN 234 487 ATP (BY SIMILARITY).  
 CC NP\_BIND 240 248



FT BINDING . 262 262 ATP (BY SIMILARITY).  
 FT ACT SITE 353 353 BY SIMILARITY.  
 FT MOD RES 382 382 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 SQ SEQUENCE 498 AA; 56513 MW; BE49D7B079FD577 CRC64;

Query Match 25.7%; Score 345.5; DB 1; Length 498;  
 Best Local Similarity 40.5%; Pred. No. 7.6e-22;  
 Matches 75; Conservative 29; Mismatches 64; Indels 17; Gaps 3;

QY 11 PPSPLSSSSVGGQGVPMTEKSKATAVAGSPAGAPALSLRGEPLTVSDGDMWTV 70  
 DB 43 PPSN-----QDDDEERFVVALPDYAAVNDRLQVLRSTGDMWMA 90  
 QY 71 LSEVSGREYNIPSVHAKVS---HGLVLEGSLREKABELLLPNEGAFILRESQTR 126  
 DB 91 RSLVTGREGVPSNFAVAPVETLEVKWFPRTISRKDAERQLLAPNKAQSFILRESBNK 150  
 QY 127 GSYSLVRLSRPASMDRIIRHYRHCILNGLYSPRLTPSPSLQALVHYSELADICLL 186  
 DB 151 GAFSLSVK-DITTOGEVVAHKINSLNGGYTSPRTTFPTLQALVQHYSKDGDCQL 209  
 QY 187 KEPCV 191  
 DB 210 TLPCV 214

RESULT 10  
 LCK\_HUMAN

ID LCK\_HUMAN STANDARD; PRT; 508 AA.  
 AC P06239; F07100; Q9NYT8; Q96DM4; Q13152; Q12850;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (P56-LCK)  
 GN (LCK) (T cell-specific protein-tyrosine kinase).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89123626; PubMed=3265417;  
 RA Perlmutter R.M., Marsh J.D., Lewis D.B., Peet R., Ziegler S.F.,  
 RA Wilson C.B.,  
 RT "Structure and expression of lck transcripts in human lymphoid  
 RT cells.";  
 RL J. Cell. Biochem. 38:117-126(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87133811; PubMed=3493153;  
 RA Koga Y., Caecia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y.,  
 RA Mak T.W.,  
 RT "A human T cell-specific cDNA clone (YT16) encodes a protein with  
 RT extensive homology to a family of protein-tyrosine kinases.";  
 RL Eur. J. Immunol. 16:1643-1646(1986).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90108697; PubMed=2558056;  
 RA Rouer E., van Huynh T., de Souza S.L., Lang M.C., Fischer S.,  
 RA Benarous R.,  
 RT "Structure of the human lck gene: differences in genomic organisation  
 RT within src-related genes affect only N-terminal exons.";  
 RL Gene 84:105-113(1989).  
 RN [4]  
 RP SEQUENCE FROM N.A., VARIANTS L-27; POKP-231 INS; V-352, L-446, AND  
 RP PHOSPHORYLATION OF TYR-393 AND TYR-504.  
 RC TISSUE=Leukemia;  
 RX MEDLINE=94187714; PubMed=8139546;  
 RA Wright D.D., Sefton B.M., Kamps M.P.,  
 RT "Oncogene activation of the lck protein accompanies translocation of  
 RT the lck gene in the human HS2 T-cell leukemia.";  
 RL Mol. Cell. Biol. 14:2429-2437(1994).

RN [5]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE=Leukemic T-cell;  
 RX MEDLINE=96085119; PubMed=7495859;  
 RA Vogel L.B., Arthur R., Fujita D.J.,  
 RT "An aberrant lck mRNA in two human T-cell lines.";  
 RL Biochim. Biophys. Acta 1264:168-172(1995).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RA Straubeberg R.,  
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE OF 13-508 FROM N.A.  
 RC TISSUE=Peripheral blood lymphocytes;  
 RX MEDLINE=20462621; PubMed=11009097;  
 RA Boncristiano W., Majolini M.B., D'Elia M.M., Pacini S., Valensin S.,  
 RA Olivieri C., Amedei A., Falini B., Del Prete G., Telford J.L.,  
 RA Baldari C.T.,  
 RT "Defective recruitment and activation of ZAP-70 in common variable  
 RT immunodeficiency patients with T cell defects.";  
 RL Eur. J. Immunol. 30:2632-2638(2000).  
 RN [8]  
 RP SEQUENCE OF 367-508 FROM N.A.  
 RX MEDLINE=88217332; PubMed=2835736;  
 RA Veilleux A., Foss F.M., Sausville E.A., Bolen J.B., Rosen N.,  
 RT "Expression of the lck tyrosine kinase gene in human colon carcinoma  
 RT and other non-lymphoid human tumor cell lines.";  
 RL Oncogene Res. 1:357-374(1987).  
 RN [9]  
 RP SEQUENCE OF 374-508 FROM N.A.  
 RX MEDLINE=87000726; PubMed=3489486;  
 RA Trevillyan J.M., Lin Y., Chen S.J., Phillips C.A., Canina C.,  
 RA Lima T.J.,  
 RT "Human T lymphocytes express a protein-tyrosine kinase homologous to  
 RT p56LCK.";  
 RL Biochim. Biophys. Acta 888:286-295(1986).  
 RN [10]  
 RP SEQUENCE OF 1-34 FROM N.A.  
 RX MEDLINE=89096891; PubMed=2850479;  
 RA Garvin A.M., Pawar S., Marsh J.D., Perlmutter R.M.,  
 RT "Structure of the murine lck gene and its rearrangement in a murine  
 RT lymphoma cell line.";  
 RL Mol. Cell. Biol. 8:3058-3064(1988).  
 RN [11]  
 RP SEQUENCE OF 1-34 FROM N.A.  
 RX MEDLINE=89313764; PubMed=2787474;  
 RA Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,  
 RA Miyamoto N.G., Mak T.W.,  
 RT "Structure of the two promoters of the human lck gene: differential  
 RT accumulation of two classes of lck transcripts in T cells.";  
 RL Mol. Cell. Biol. 9:2173-2180(1989).  
 RN [12]  
 RP MASS SPECTROMETRY.  
 RC TISSUE=Breast cancer;  
 RX MEDLINE=21829512; PubMed=11840567;  
 RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,  
 RA Patch R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,  
 RA Zvelebil M.J.,  
 RT "Cluster analysis of an extensive human breast cancer cell line  
 RT protein expression map database.";  
 RL Proteomics 2:212-223(2002).  
 RN [13]  
 RP INTERACTION WITH PI3K.  
 RX MEDLINE=94067101; PubMed=7504174;  
 RA Vogel L.B., Fujita D.J.,  
 RT "The SH2 domain of p56lck is involved in binding to  
 RT phosphatidylinositol 3'-kinase from T lymphocytes.";  
 RL Mol. Cell. Biol. 13:7408-7417(1993).  
 RN [14]  
 RP INTERACTION WITH KHDRBS1.  
 RX MEDLINE=9515308; PubMed=7852312;  
 RA Vogel L.B., Fujita D.J.,





Db 211 ASDGLCTKLSRPCQTK 227

RESULT 12

LCCK\_CHICK STANDARD; PRT; 507 AA.

AC P42683;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Proco-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (Protein-tyrosine kinase C-TKL).

GN LCK.

OS Gallus gallus (chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

OC NCBI\_TaxID=9031;

OX [1]

RN SEQUENCE OF 1-88 FROM N.A.

RP MEDLINE=8097370; PubMed=1545804;

RX Chow L., Ratcliffe M., Velllette A.

RT "Lck is the avian homolog of the mammalian lck tyrosine protein kinase gene."

RL Mol. Cell. Biol. 12:1226-1233(1992).

RN [2]

RP SEQUENCE OF 46-507 FROM N.A.

RX MEDLINE=8097370; PubMed=3321053;

RA Strephardt K., Mullins J.I., Bruck C., Ruebsamen-Waigmann H.

RT "Additional member of the protein-tyrosine kinase family: the src- and lck-related protooncogene c-tkl."

RL Proc. Natl. Acad. Sci. U.S.A. 84:8778-8782(1987).

CC -1- FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.

CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

CC -1- SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER CD4 OR CD8.

CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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CC -----

DR EMBL; M85043; AAA49003.1; -

DR EMBL; J03579; AAA49081.1; ALT\_INIT.

DR HSPB; P06239; 3LCK.

DR InterPro: IPR000719; Euk\_pkinase.

DR InterPro: IPR000980; SH2.

DR InterPro: IPR001452; SH3.

DR InterPro: IPR001245; Tyr\_pkinase.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3; 1.

DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00401; SH2DOMAIN.

DR PRINTS; PR00452; SH3DOMAIN.

DR PRINTS; PR00109; TYRKINASE.

DR Prodom; PD000001; Euk\_pkinase; 1.

DR Prodom; PD000066; SH2; 1.

DR Prodom; PD000093; SH3; 1.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00326; SH3; 1.

DR SMART; SM00219; Tyrc; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.

DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS50001; SH2; 1.

DR PROSITE; PS50002; SH3; 1.

KW Proco-oncogene; Tyrosine-protein kinase; Phosphorylation; Transferase;

KW ATP-binding; Myristate; SH2 domain; SH3 domain; Palmitate;

KW Lipoprotein.

FT INIT MET 0 0 PROBABLE.

FT LIPID 1 1 MYRISTATE (BY SIMILARITY).

FT LIPID 2 2 PALMITATE (BY SIMILARITY).

FT LIPID 4 4 PALMITATE (BY SIMILARITY).

FT LIPID 59 119 SH3.

FT DOMAIN 125 222 SH2.

FT DOMAIN 243 496 PROTEIN KINASE.

FT NP BIND 249 257 ATP (BY SIMILARITY).

FT BINDING 271 271 ATP (BY SIMILARITY).

FT ACT SITE 362 362 BY SIMILARITY.

FT MOD\_RES 392 392 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

FT MOD\_RES 503 503 PHOSPHORYLATION (NEGATIVE REGULATION) (BY SIMILARITY).

FT SEQUENCE 507 AA; 58008 MW; BC83CF8A9186170 CRC64;

Query Match 25.0%; Score 337; DB 1; Length 507;

Best Local Similarity 43.8%; Pred. No. 4.1e-21;

Matches 71; Conservative 27; Mismatches 60; Indels 4; Gaps 1;

Db 37 VALGSPAGAPAEPLRLGPEPLTVSESDGDMWTVSEVSGREYVPSVAVAKVSG---HG 92

65 VALVDYPTDGLDGLKQCEKRLVRESGEMWRAQSITTCQEGILPNNFVAVWNSLLEPEP 124

93 WLVEGLSREKAEELLPLPENGCAFLIRSQTRRSGSYLSVRLSPASNDRIHRIRICL 152

125 WFKMGLYSRKAERALLASGNTGSGFLIRSETSKSYSLVRDDQNGQTVYKIRNM 184

Qy 153 DNGMGLYSRPTLPSLQALVDHYSELADICCLLKSPCVLOR 194

185 DNGGYISPRVYTSLSHLVEYSSSDGCLTRKGPCKRHX 226

Db 185 DNGGYISPRVYTSLSHLVEYSSSDGCLTRKGPCKRHX 226

RESULT 13

ID YES\_XENLA STANDARD; PRT; 537 AA.

AC P10346;

DT 01-JUL-1989 (Rel. 11, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Proco-oncogene tyrosine-protein kinase YES (EC 2.7.1.112) (6e1-YES) (C-YES).

GN YES.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus.

OC NCBI\_TaxID=8155;

OX [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=89296347; PubMed=2472592;

RX Steele R.E., Irwin M.Y., Knudsen C.L., Collect J.W., Fero J.B.

RT "The yes proto-oncogene is present in amphibians and contributes to the maternal RNA pool in the oocyte."

RL Oncogene Res. 4:223-233(1989).

CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.

CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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CC -----

EMBL: X14377; CAJ32551.1; -  
 PIR: S08517; S08517.  
 DR HSSP: P00523; 2PTK.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR000980; SH2.  
 DR InterPro: IPR001452; SH3.  
 DR InterPro: IPR01245; Tyr\_pkinase.  
 DR Pfam: PF00017; SH2; 1.  
 DR Pfam: PF00018; SH3; 1.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PR00401; SH2DOMAIN.  
 DR PRINTS: PR00452; SH3DOMAIN.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR ProDom: PD000066; SH3; 1.  
 DR ProDom: PD000093; SH2; 1.  
 DR SMART: SM00252; SH2; 1.  
 DR SMART: SM00326; SH3; 1.  
 DR SMART: SM00219; TYRK; 1.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS50001; SH2; 1.  
 DR PROSITE: PS50002; SH3; 1.  
 DR Proto-oncogene; Tyrosine-protein kinase; Phosphorylation; Transferrase; ATP-binding; Myristate; SH3 domain; SH2 domain.  
 KW TRANSFERRASE; ATP-BINDING; MYRISTATE (BY SIMILARITY).  
 FT LIPID 2 2  
 FT DOMAIN 85 146 SH3.  
 FT DOMAIN 152 249 SH2.  
 FT DOMAIN 271 524 PROTEIN KINASE.  
 FT NP\_BIND 277 285 ATP (BY SIMILARITY).  
 FT BINDING 299 299 ATP (BY SIMILARITY).  
 FT ACT\_SITE 390 390 BY SIMILARITY.  
 FT MOD\_RES 420 420 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 SQ SEQUENCE 537 AA; 60357 MW; F26F615940AC1B CRC64;

Query Match 24.0%; Score 323.5; DB: 1; Length 537;  
 Best Local Similarity 33.6%; Pred. No. 6, 2e-20;  
 Matches 85; Conservative 38; Mismatches 91; Indels 39; Gaps 7;

37 VALGSPAGGPAELSLRLGEPPLTVSE-DGDWTVLSEVSGREYINPSVHAKV-----SH 91  
 91 VALYDEARTTEDSPFKRGRFQIINTEGDWEARSIAITGKTGYIPSNVYAPADSIQGE 150

92 GMLYEGLSREKAEELLPLPBGGAFLIREQSOTRGYSLSVRLSRPMRR-----H 146  
 151 EWYFGMGKRAEELPLNPQNGRTFLVRESEITKAGYLSLR-----DWDEVRGDNVZH 205

147 YRIHLCDNGMLYISPRLLTFPSLQALVDHYSELADLICLLKEPC-----VLGRAP 197  
 206 YKIRKLNDNGYVITTRAQFESLQKVKHYSEHADGLCYRLTTVCPSVKPTQGLADAME 265

198 LPGKDIPLPVIVOR-----TPLNWKELDSSLSEKATGEESLSSEGLARS 243  
 266 IPRFESRLDVLKGGCGCGEAVIGTWNGTTKVAIKTLTKPGTMPEAFLOEAQIMKURHDK 325

244 L-SFYTSLNDEAV 255  
 326 LVPLVAVVSEEP 338

RESULT 14  
 YES\_CHICK  
 ID YES\_CHICK STANDARD; PRT; 541 AA.  
 AC P09324;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Proto-oncogene tyrosine-protein kinase YES (EC 2.7.1.112) (P61-YES) (C-YES).  
 GN YES.  
 OS Gallus gallus (chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=69041591; PubMed=3054816;  
 RA Sudol M., Kleswetter C., Zhao Y.H., Doral T., Wang L.H., Hanafusa H.;  
 RT "Nucleotide sequence of a cDNA for the chick yes proto-oncogene: comparison with the viral yes gene."  
 RL Nucleic Acids Res. 16:9876-9876(1988).  
 RN [2]  
 RP REVISED TO 232.  
 RA Sudol M.;  
 RL Submitted (NOV-1988) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney, and Brain;  
 RX MEDLINE=89128204; PubMed=2464785;  
 RA Zheng X., Podell S., Sefton B.M., Kaplan P.L.;  
 RT "The sequence of chicken C-yes and p61c-yes";  
 RL Oncogene 4:99-104(1989).  
 RN [4]  
 RP SEQUENCE OF 396-451 FROM N.A.  
 RX MEDLINE=93096482; PubMed=1281306;  
 RA Marcelle C., Richmann A.;  
 RT "Molecular cloning of a family of protein kinase genes expressed in the avian embryo."  
 RL Oncogene 7:2479-2487(1992).  
 CC -I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.  
 CC -I- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.  
 CC -I- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -I- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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CC EMBL: X1207; CAJ3195.1; -  
 CC EMBL: X12461; CAJ31002.1; -  
 CC EMBL: X69695; CAJ49365.1; -  
 CC PIR: S03324; TVCHYS.  
 CC HSSP: P00523; 2PTK.  
 CC InterPro: IPR000719; Euk\_pkinase.  
 CC InterPro: IPR000980; SH2.  
 CC InterPro: IPR001452; SH3.  
 CC InterPro: IPR01245; Tyr\_pkinase.  
 CC Pfam: PF00017; SH2; 1.  
 CC Pfam: PF00018; SH3; 1.  
 CC Pfam: PF00069; pkinase; 1.  
 CC PRINTS: PR00401; SH2DOMAIN.  
 CC PRINTS: PR00452; SH3DOMAIN.  
 CC PRINTS: PR00109; TYRKINASE.  
 CC ProDom: PD000001; Euk\_pkinase; 1.  
 CC ProDom: PD000066; SH3; 1.  
 CC ProDom: PD000093; SH2; 1.  
 CC SMART: SM00252; SH2; 1.  
 CC SMART: SM00326; SH3; 1.  
 CC SMART: SM00219; TYRK; 1.  
 CC PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
 CC PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 CC PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC PROSITE: PS50001; SH2; 1.  
 CC PROSITE: PS50002; SH3; 1.  
 CC Proto-oncogene; Tyrosine-protein kinase; Phosphorylation; Transferrase; ATP-binding; Myristate; SH3 domain; SH2 domain.  
 KW TRANSFERRASE; ATP-BINDING; MYRISTATE (BY SIMILARITY).  
 FT LIPID 2 2  
 FT DOMAIN 85 146 SH3.  
 FT DOMAIN 152 249 SH2.  
 FT DOMAIN 271 524 PROTEIN KINASE.  
 FT NP\_BIND 277 285 ATP (BY SIMILARITY).  
 FT BINDING 299 299 ATP (BY SIMILARITY).  
 FT ACT\_SITE 390 390 BY SIMILARITY.  
 FT MOD\_RES 420 420 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 SQ SEQUENCE 537 AA; 60357 MW; F26F615940AC1B CRC64;

FT DOMAIN 89 150 SH3.  
 FT DOMAIN 156 253 SH2.  
 FT DOMAIN 275 528 PROTEIN KINASE.  
 FT NP BIND 281 289 ATP (BY SIMILARITY).  
 FT BINDING 303 303 ATP (BY SIMILARITY).  
 FT ACT SITE 394 394 BY SIMILARITY.  
 FT MOD\_RBS 424 424 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT CONFLICT 67 71 TPEGG -> IHPK (IN REF. 3).  
 FT CONFLICT 82 82 P -> Q (IN REF. 3).  
 SQ SEQUENCE 541 AA; 60792 MW; BEA849CCTD1755AF CRC64;  
 Query Match 23.8%; Score 321; DB 1; Length 541;  
 Best Local Similarity 31.8%; Pred. No. 1e-19;  
 Matches 92; Conservative 43; Mismatches 104; Indels 50; Gaps 9;

QY 1 GSLSRRKSLPPSSLSVGGQGPVMEERSKATVALGSPFAGPAELSLRLEPLTI 60  
 DB 70 GGAASSPSAVSPSPSTLT--GGVTV-----FVALDYEARFTDLSFKGGERFOI 118  
 QY 61 VSE-DGDMWTVLSEVSGREYVNPVAVAKV---SHGMYEGSRKABELLLPGNPGC 115  
 DB 119 INTEGDMWEARSINTGKTGYISNYVAPADSIQAEKYGKGRKDAERLLNPGNQG 178  
 QY 116 AFLIRSQTRGSGYSLVRLSPASDRIR----HRIHCLDNGMLYISPLTFEPLQ 170  
 DB 179 IFVRSSETTKGAVSLIR-----DWDEVGDNVYKIRKLDNGGYITTRAFESLQK 233  
 QY 171 LVHVELADIDICCLLEKPC-----VLQRAGPLGKDIPLPTVQR----- 211  
 DB 234 LVHGREHADGICHLTTCVCTVPGTQGLAKDAKEIPRESLLEFKAGQCGFGEVMGT 233  
 QY 212 ----TPLNKKEIDSSLSLFEANAGESLSISGLRSL-SFYISLNDVAN 255  
 DB 294 WNGTTVAIKTLKPGTMMPEAFLOEAMKRLRHDKLVPLAVVSEPT 342

RESULT 15  
 ID\_FYIN HUMAN STANDARD; PRT; 536 AA.  
 AC P06241;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Proto-oncogene tyrosine-protein kinase FYN (EC 2.7.1.112) (P59-FYN)  
 DE (SYN) (SLK).  
 DE FYN.  
 GN FYN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=66287278; PubMed=526330;  
 RA Samba K., Nishizawa M., Miyajima N., Yoshida M.C., Sukegawa J.,  
 RA Yamashiki Y., Sasaki M., Yamamoto T., Toyoshima K.,  
 RA "Yes-related protooncogene, syn. belongs to the protein-tyrosine  
 RT kinase family.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5459-5463(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=87089775; PubMed=3099169;  
 RA Kawakami T., Pennington C.Y., Robbins K.C.;  
 RT "Isolation and oncogenic potential of a novel human src-like gene.";  
 RL Mol. Cell. Biol. 6:4195-4201(1986).  
 RN [3]  
 RP MYRISTOYLATION, AND PHOSPHORYLATION OF TYR-530.  
 RA MEDLINE=91016431; PubMed=1699196;  
 RA Peters D.J., McGrew B.R., Perron D.C., Lipyak L.M., Laudano A.P.;  
 RT "In vivo phosphorylation and membrane association of the fyn proto-  
 oncogene product in IM-9 human lymphoblasts.";  
 RL Oncogene 5:1313-1319(1990).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF SH3 DOMAIN.

RX MEDLINE=93327750; PubMed=7687536;  
 RA Noble M.E.M., Musacchio A., Saraste M., Courtneidge S.A.,  
 RA Wiernenga R.K.;  
 RT "Crystal structure of the SH3 domain in human Fyn; comparison of the  
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 RT spectrin.";  
 RL EMBO J. 12:2617-2624(1993).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 80-141.  
 RA MEDLINE=95393198; PubMed=7664083;  
 RA Musacchio A., Saraste M., Williams M.;  
 RT "High-resolution crystal structures of tyrosine kinase SH3 domains  
 RT complexed with proline-rich peptides.";  
 RL Nat. Struct. Biol. 1:546-551(1994).  
 RN [6]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 84-140 IN COMPLEX WITH NEF.  
 RA MEDLINE=96279837; PubMed=8681387;  
 RA Lee C.H., Saksela K., Mirza U.A., Chait B.T., Kuriyan J.;  
 RT "Crystal structure of the conserved core of HIV-1 Nef complexed with  
 RT a Src family SH3 domain.";  
 RL Cell 85:931-942(1996).  
 RN [7]  
 RP STRUCTURE BY NMR OF SH3 DOMAIN.  
 RA MEDLINE=96399716; PubMed=8805554;  
 RA Morton C.V., Fugh D.V.R., Brown E.L.J., Kahmann J.D., Renzoni D.A.C.,  
 RA Campbell I.D.;  
 RT "Solution structure and peptide binding of the SH3 domain from human  
 RT Fyn.";  
 RL Structure 4:705-714(1996).  
 RN [8]  
 RP STRUCTURE BY NMR.  
 RA MEDLINE=97121261; PubMed=8961927;  
 RA Renzoni D.A., Fugh D.V., Siligardi G., Das P., Morton C.J., Rossi C.,  
 RA Waterfield M.D., Campbell I.D., Ladbury J.E.;  
 RT "Structural and thermodynamic characterization of the interaction of  
 RT the SH3 domain from Fyn with the proline-rich binding site on the p85  
 RT subunit of PI3-kinase.";  
 RL Biochemistry 35:15646-15653(1996).  
 RN [9]  
 RP STRUCTURE BY NMR OF SH2 DOMAIN.  
 RA MEDLINE=98035454; PubMed=9351806;  
 RA Mulhern T.D., Shaw G.L., Morton C.J., Day A.J., Campbell I.D.;  
 RT "The SH2 domain from the tyrosine kinase Fyn in complex with a  
 RT phosphotyrosyl peptide reveals insights into domain stability and  
 RT binding specificity.";  
 RL Structure 5:1313-1323(1997).  
 RN [10]  
 RP BINDING OF SH3 DOMAIN TO PI 3-KINASE.  
 RA MEDLINE=93348274; PubMed=8394019;  
 RA Prasad K.V., Janssen O., Kapeller R., Raab M., Cantley L.C.,  
 RA Rudd C.E.;  
 RT "Src-homology 3 domain of protein kinase p59fyn mediates binding to  
 RT phosphatidylinositol 3-kinase in T cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7366-7370(1993).  
 CC -1- FUNCTION: IMPLICATED IN THE CONTROL OF CELL GROWTH.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBUNIT: ASSOCIATES THROUGH ITS SH3 DOMAIN TO THE P85 SUBUNIT OF  
 CC PHOSPHATIDYLINOSITOL 3-KINASE. INTERACTS WITH THE FYN-BINDING  
 CC PROTEIN (FYN).  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
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